

FIG. 1

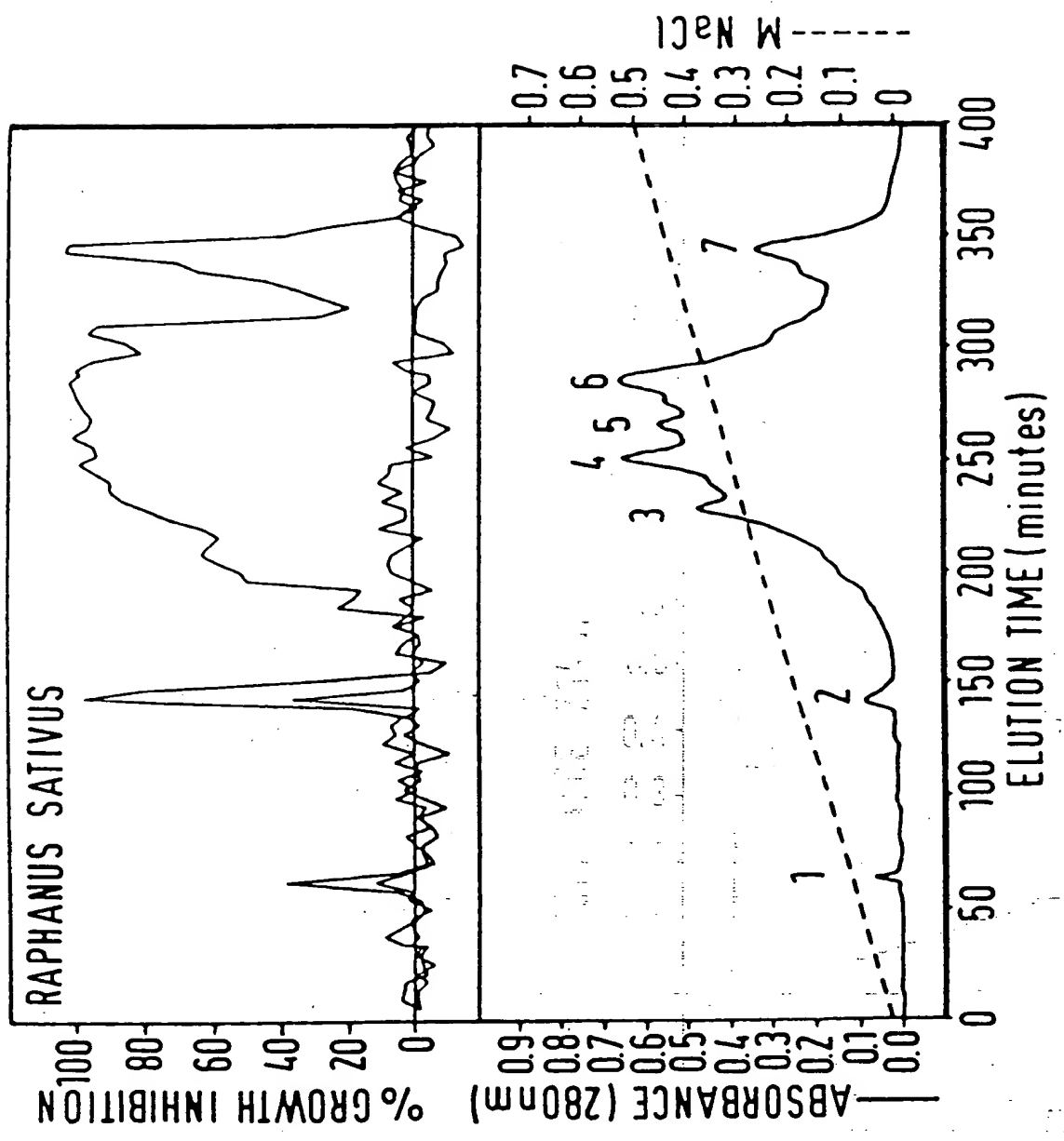


FIG. 2A

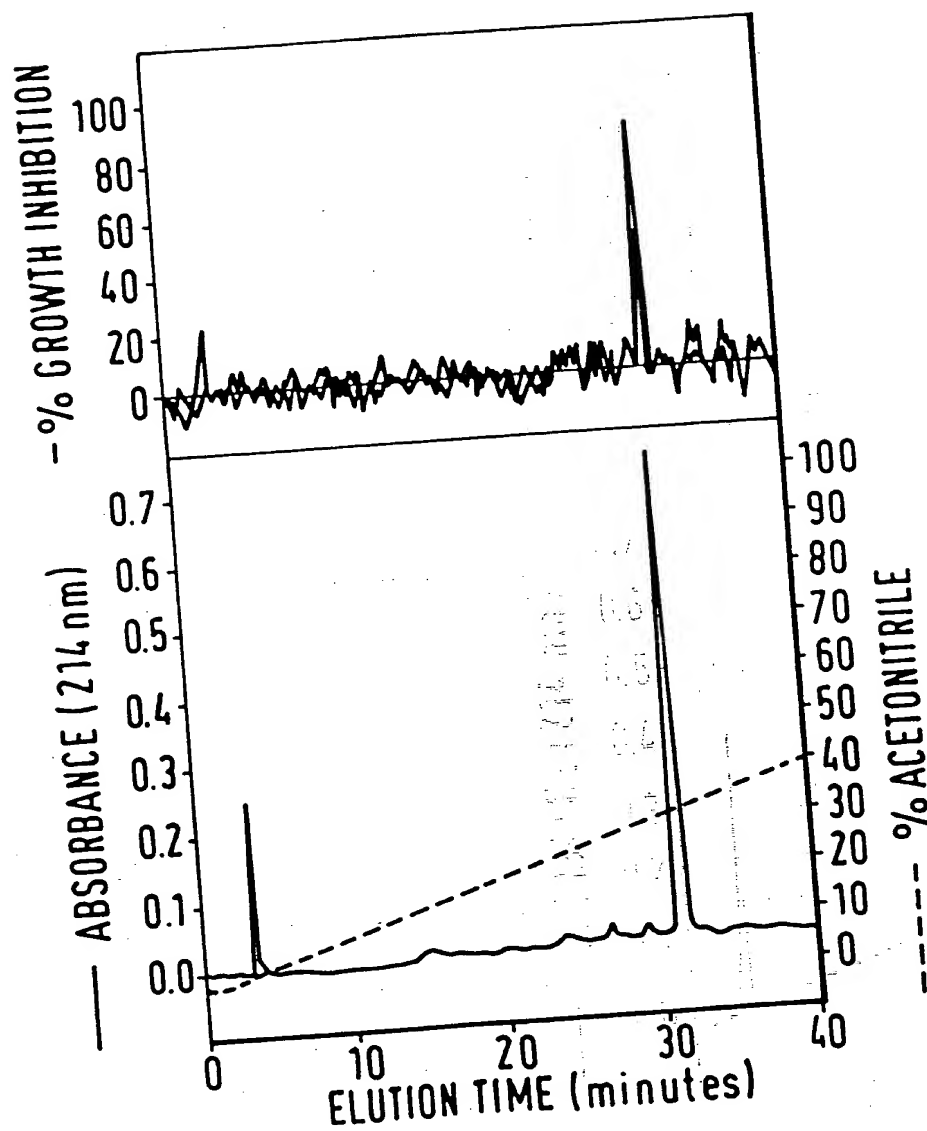


FIG. 2B

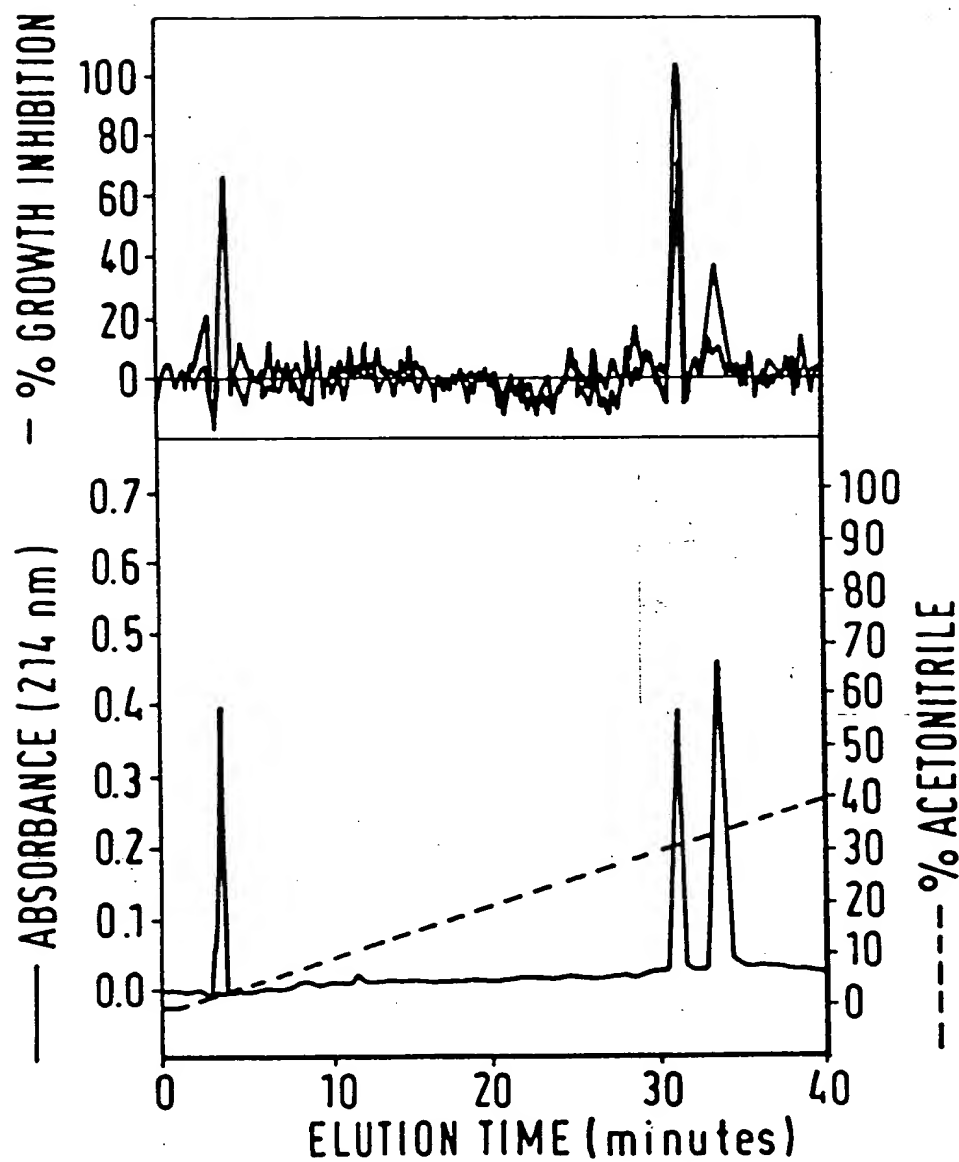
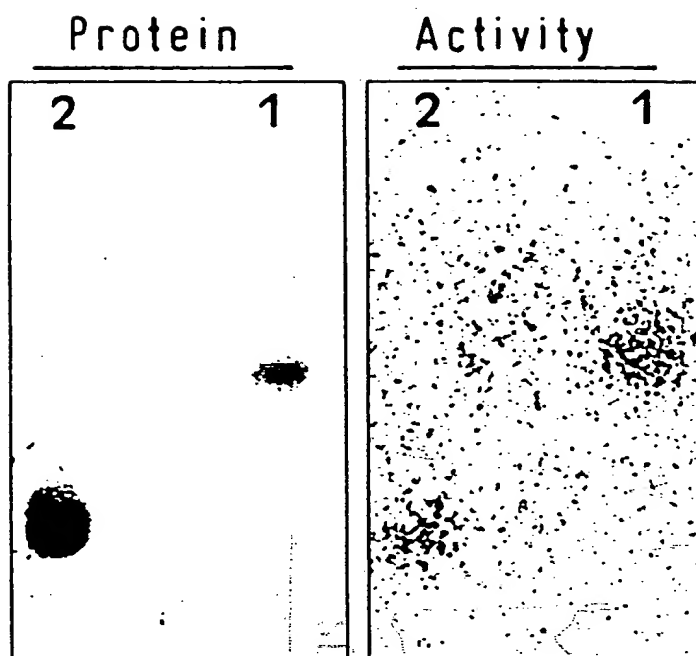


FIG. 3



102110 18565260

FIG. 4

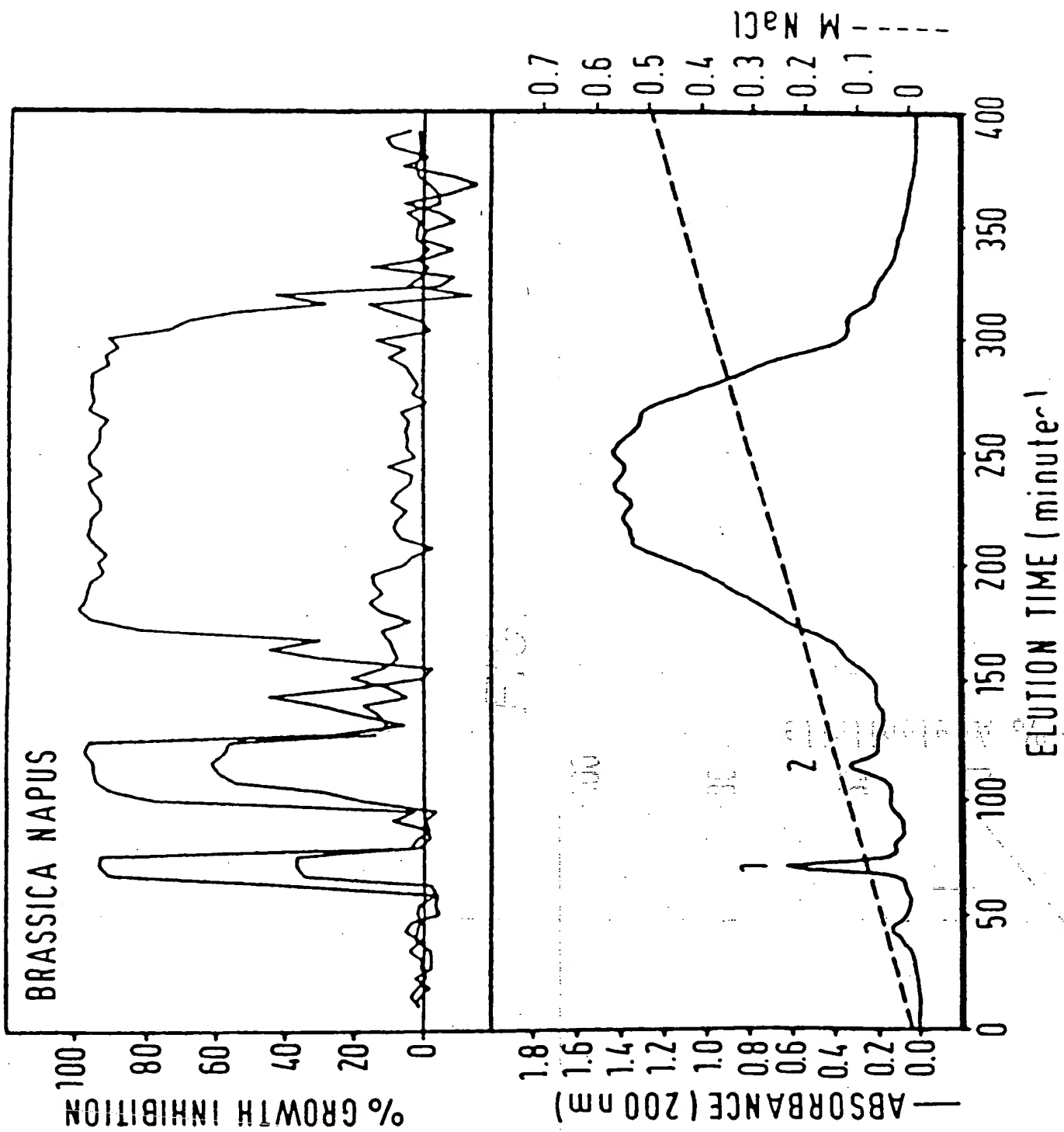
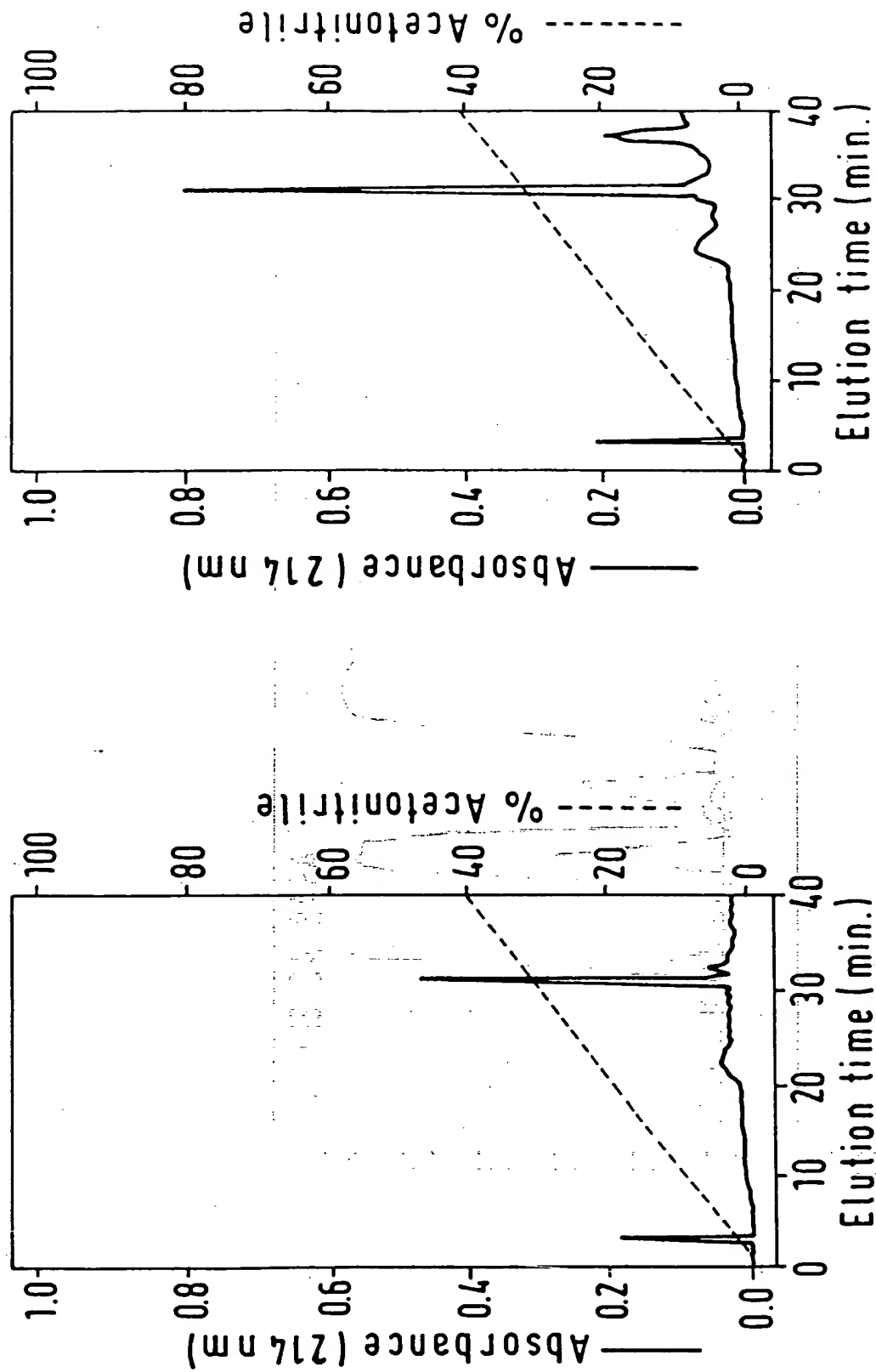


FIG. 5



TOPTO-10565260

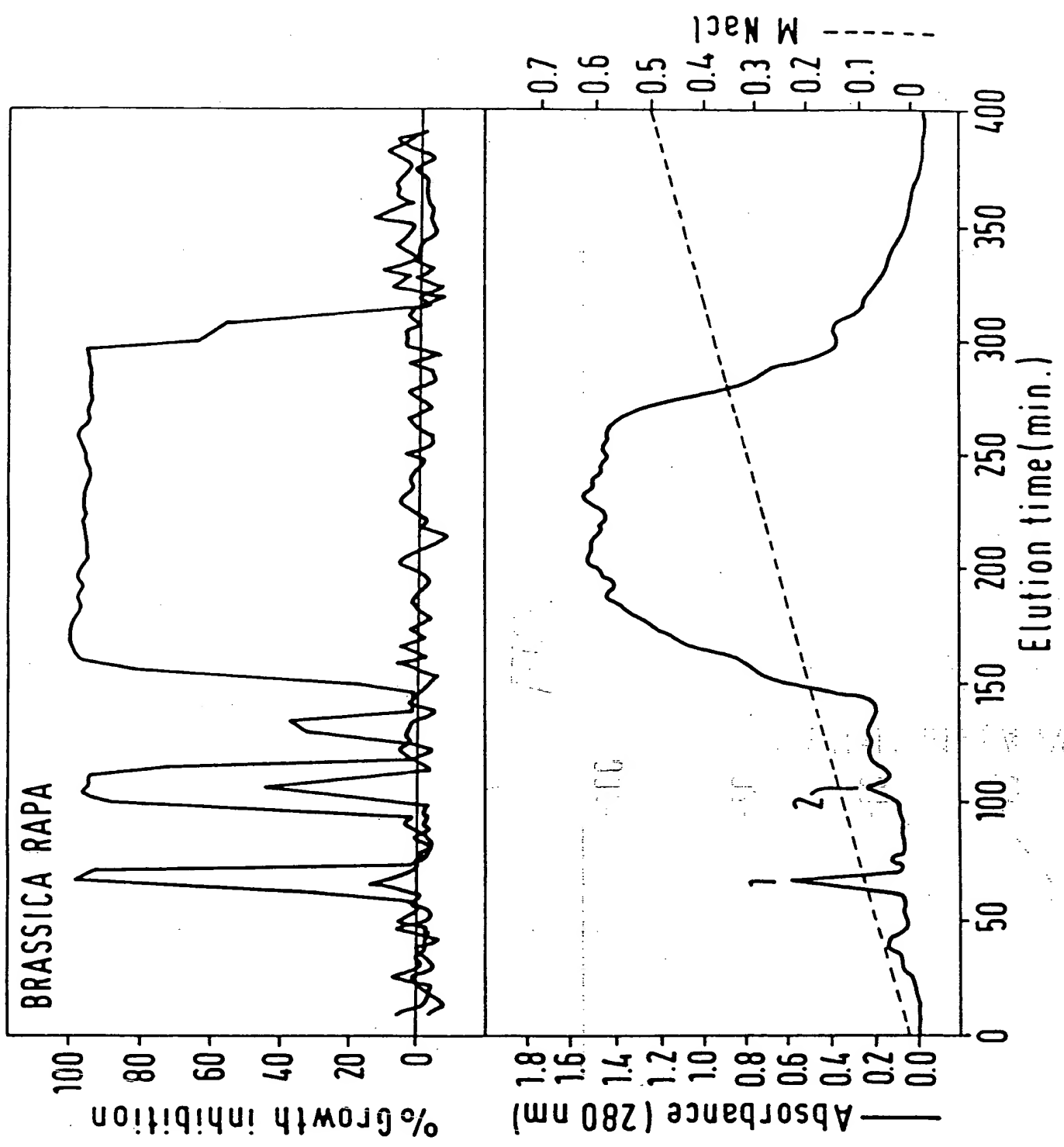


FIG. 6

00210 4830444

FIG. 7

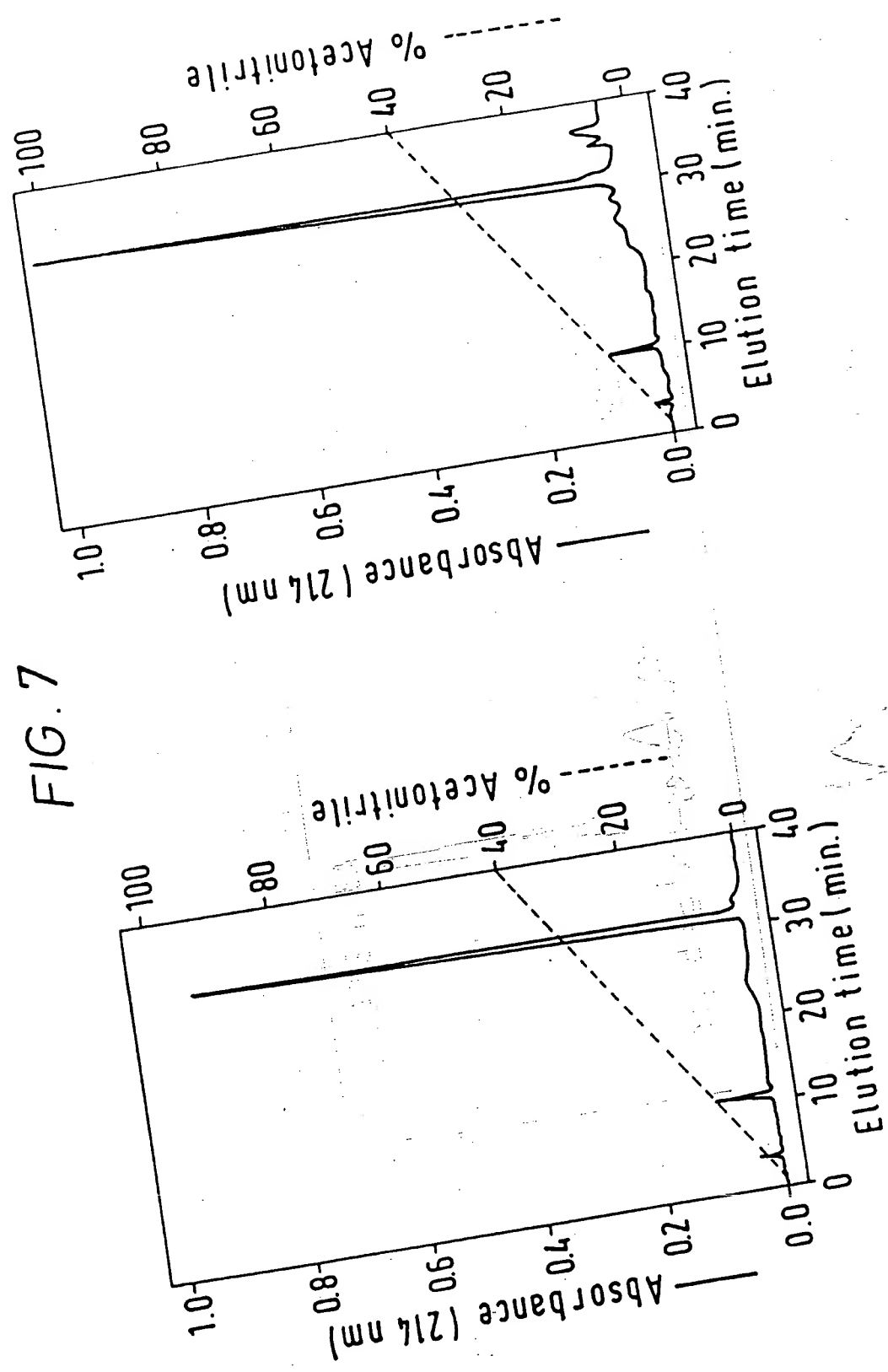




FIG. 8

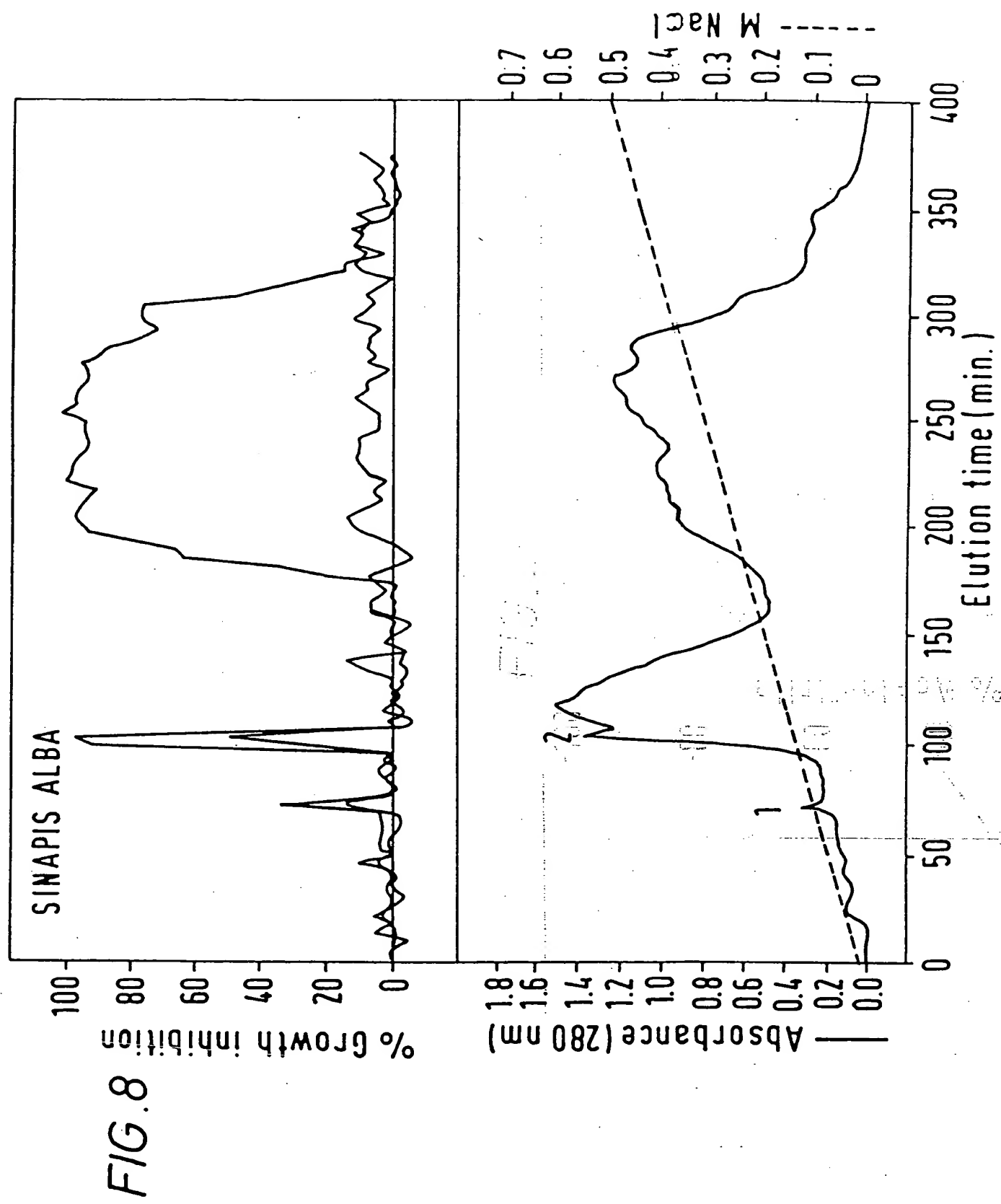


FIG. 9

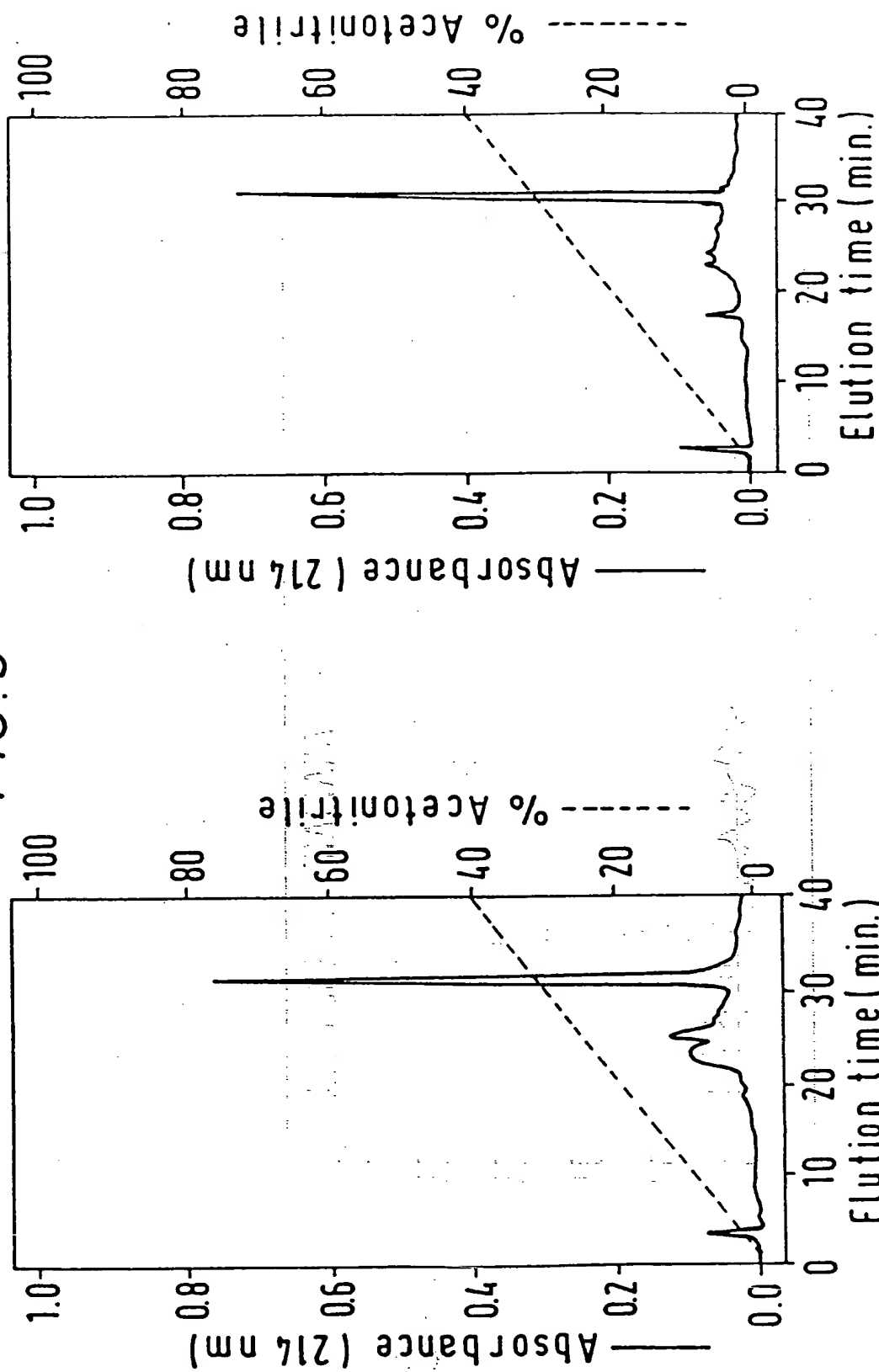


FIG.10

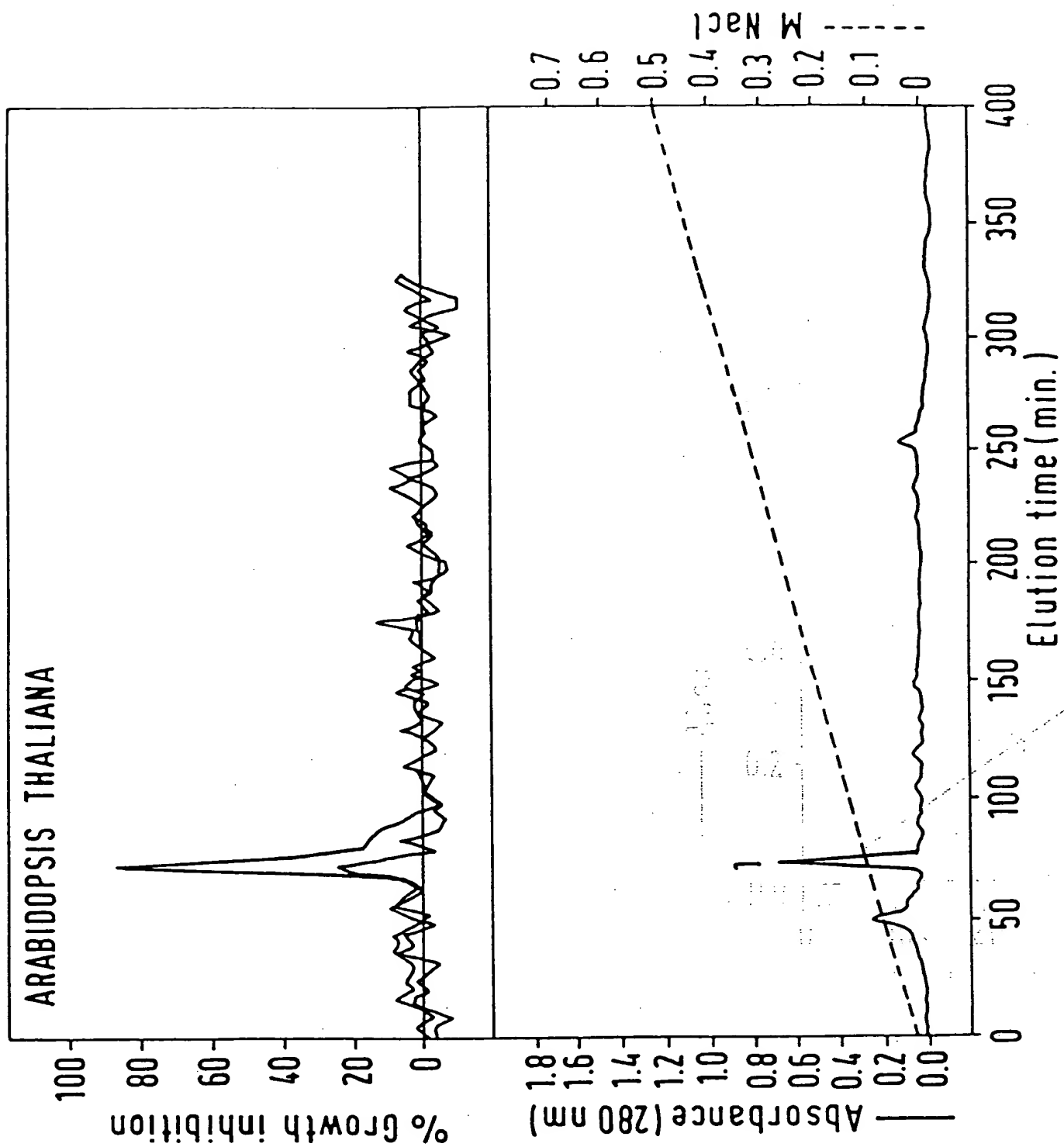


FIG. 11

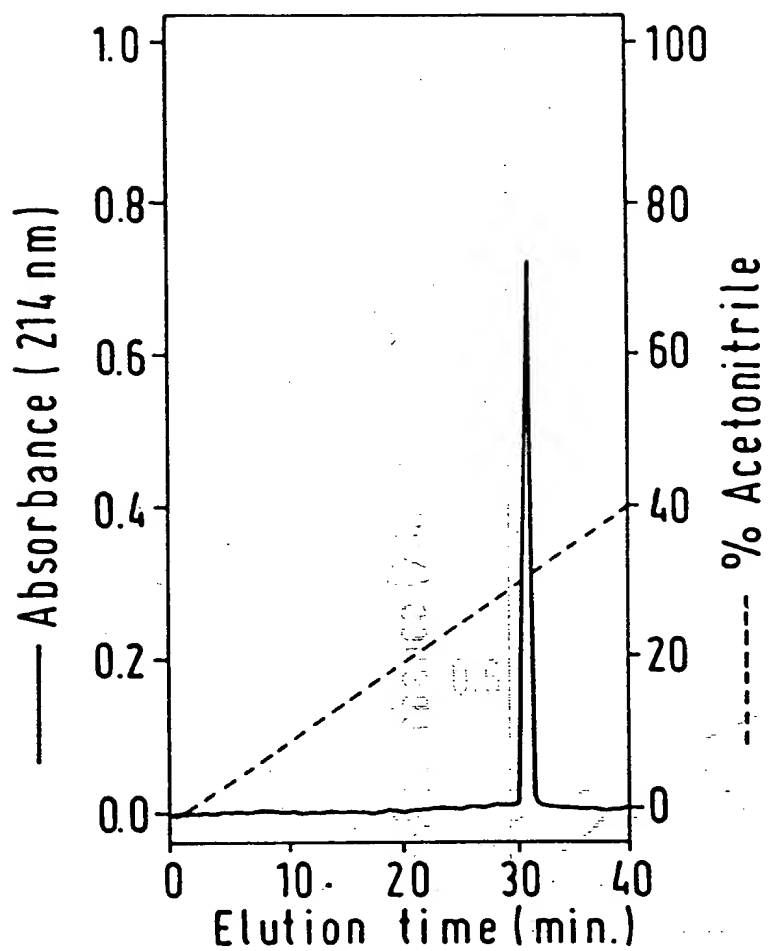


FIG. 12

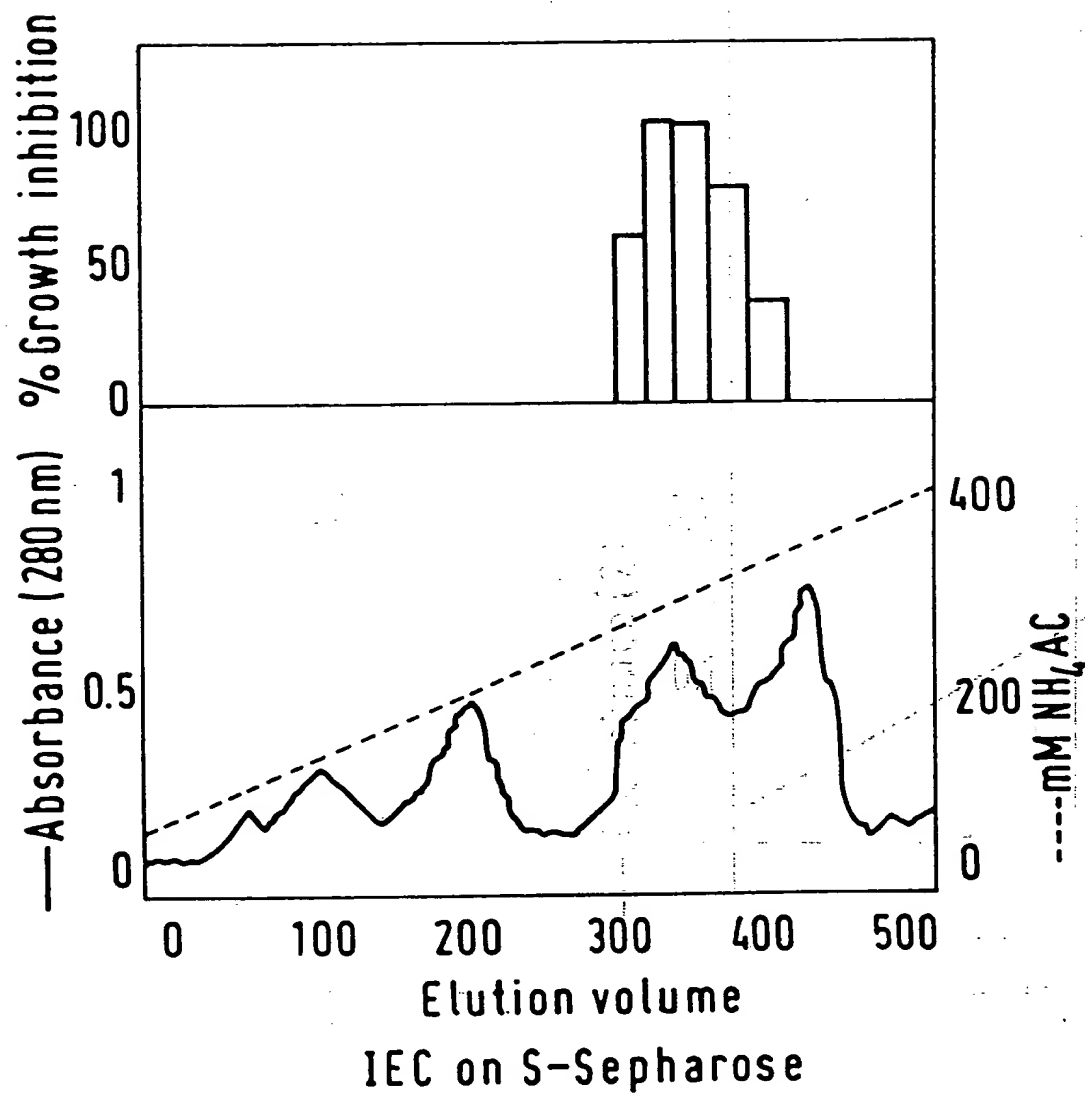


FIG. 13

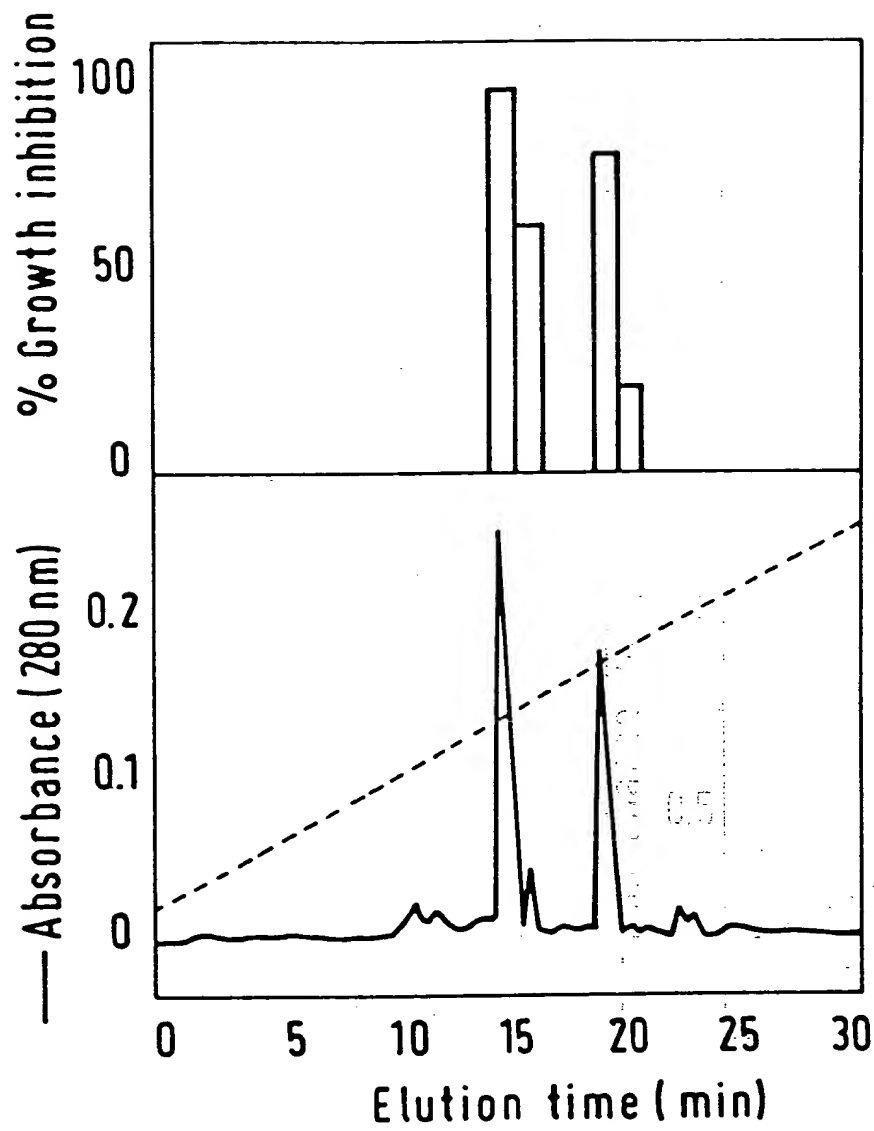


FIG. 14

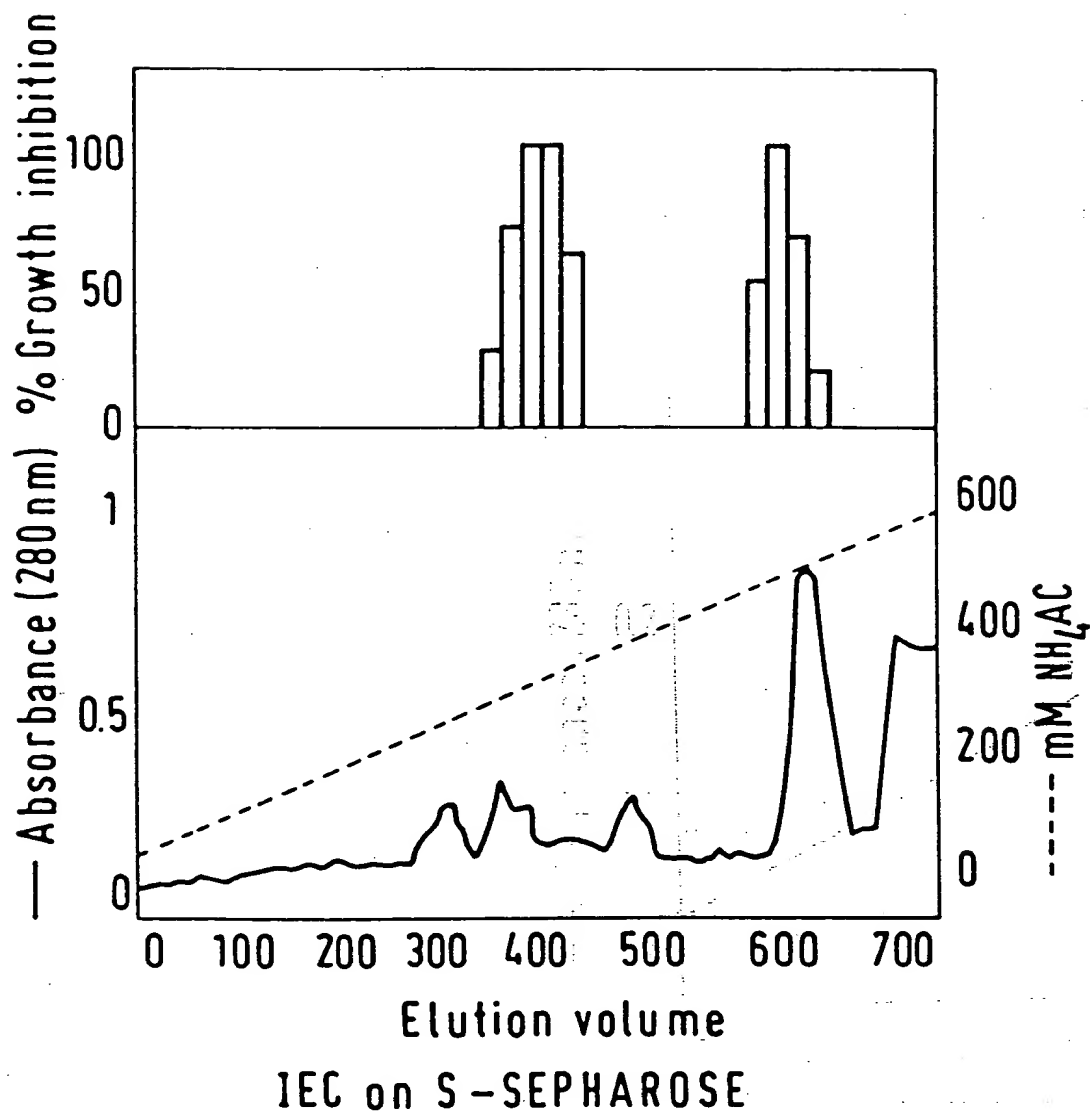


FIG.15

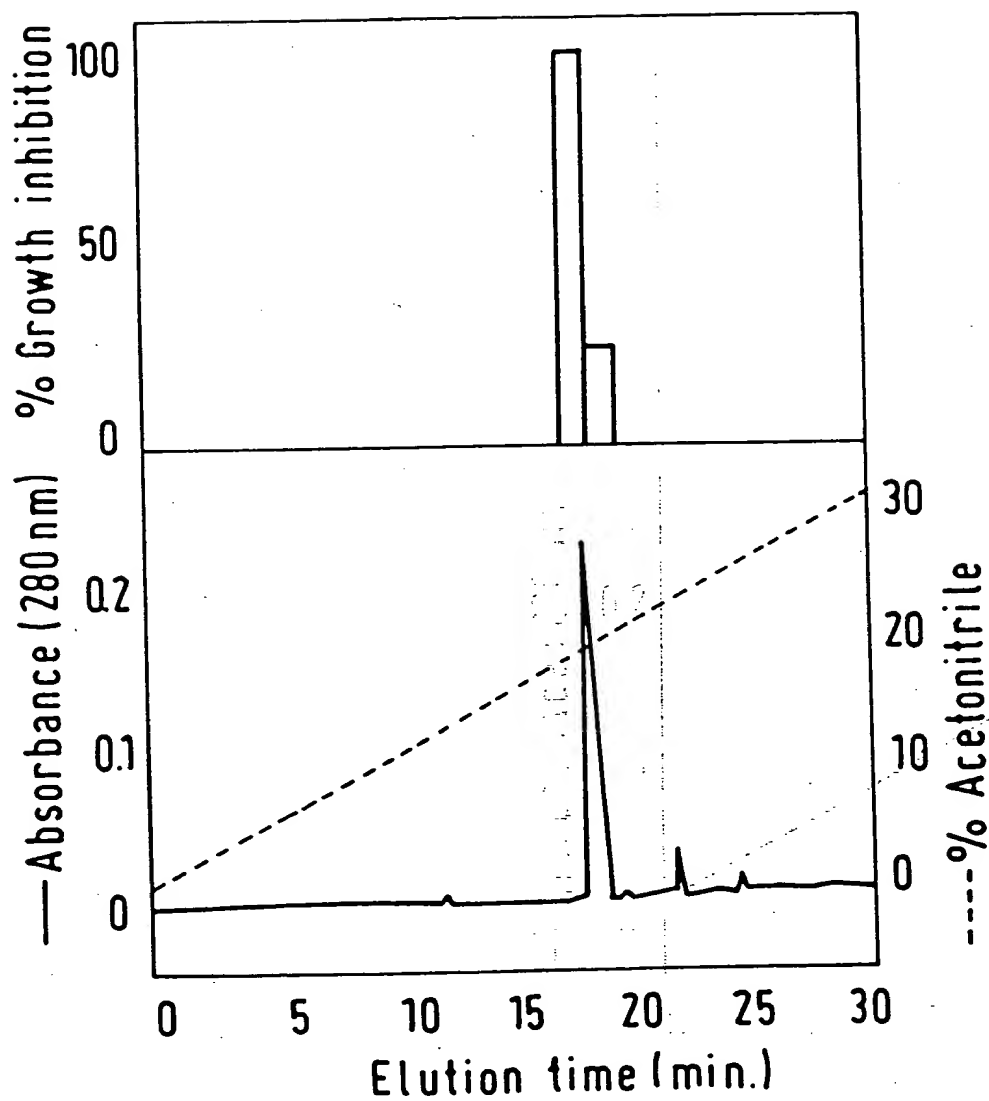




FIG. 16

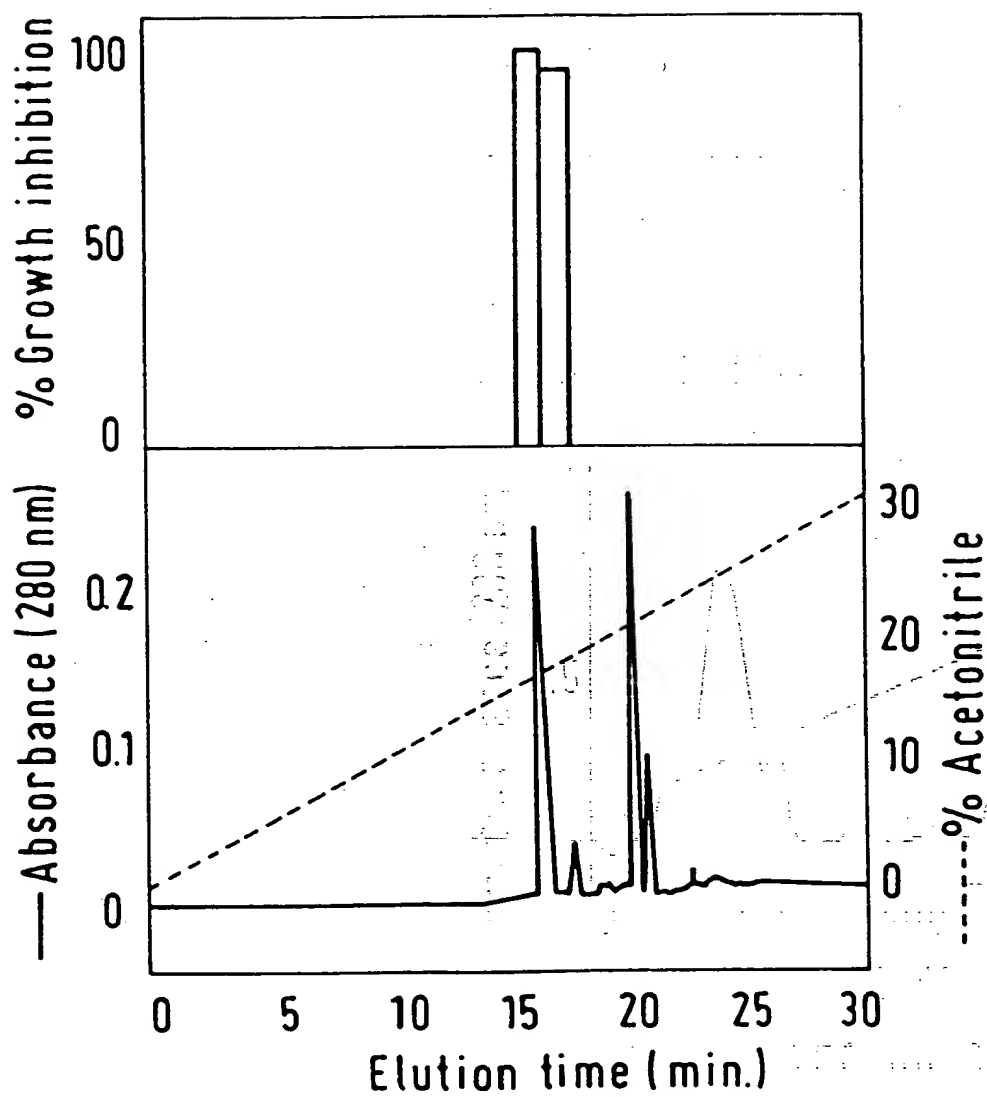


FIG. 17

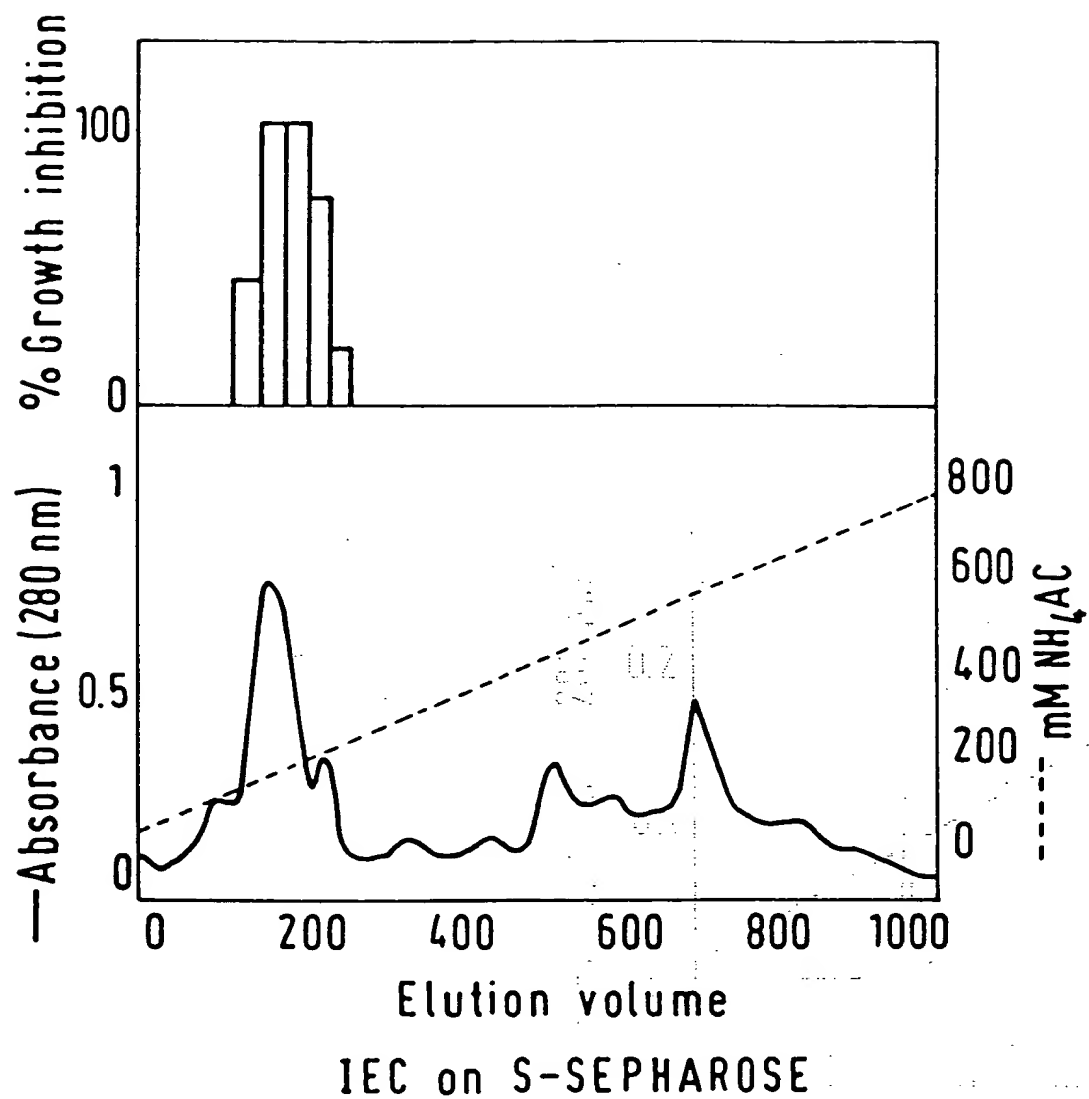


FIG. 18

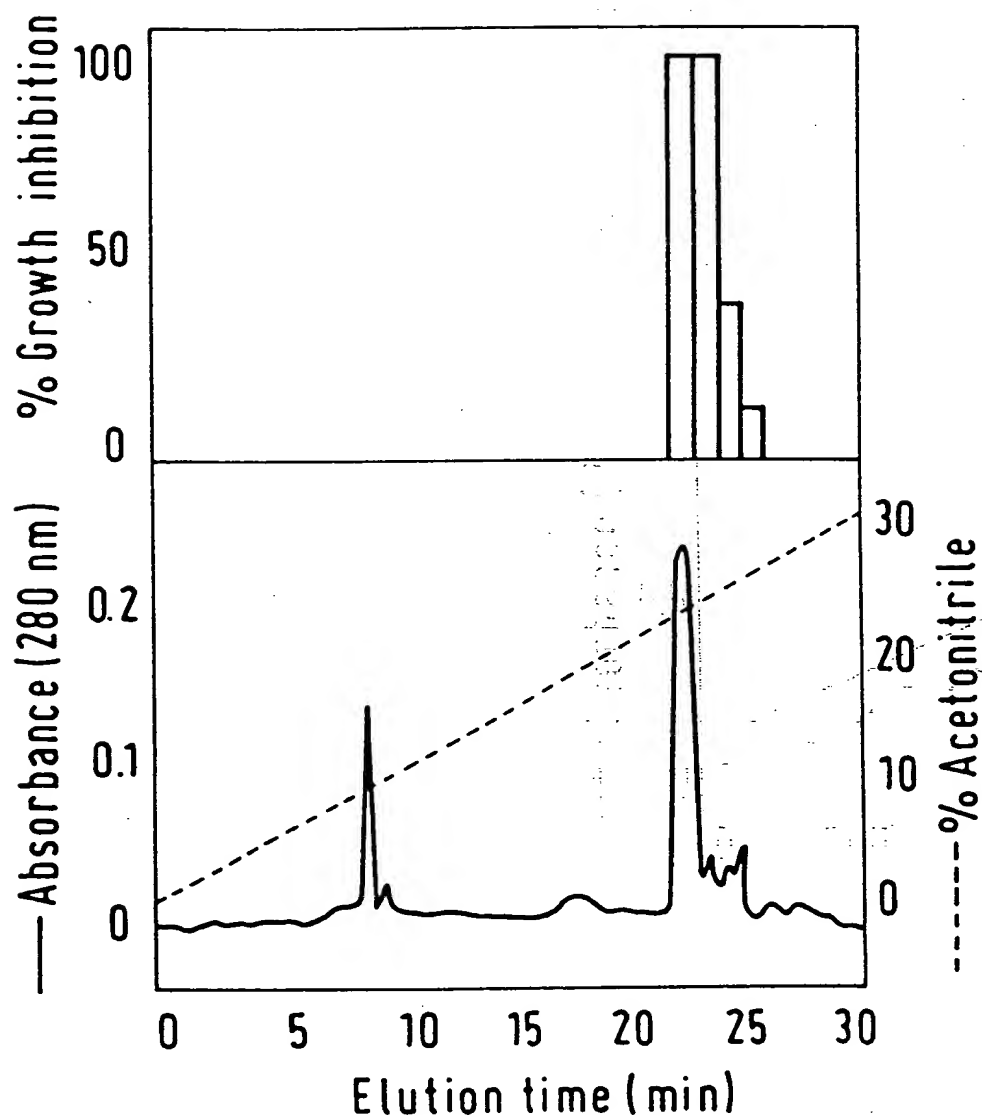


FIG. 19

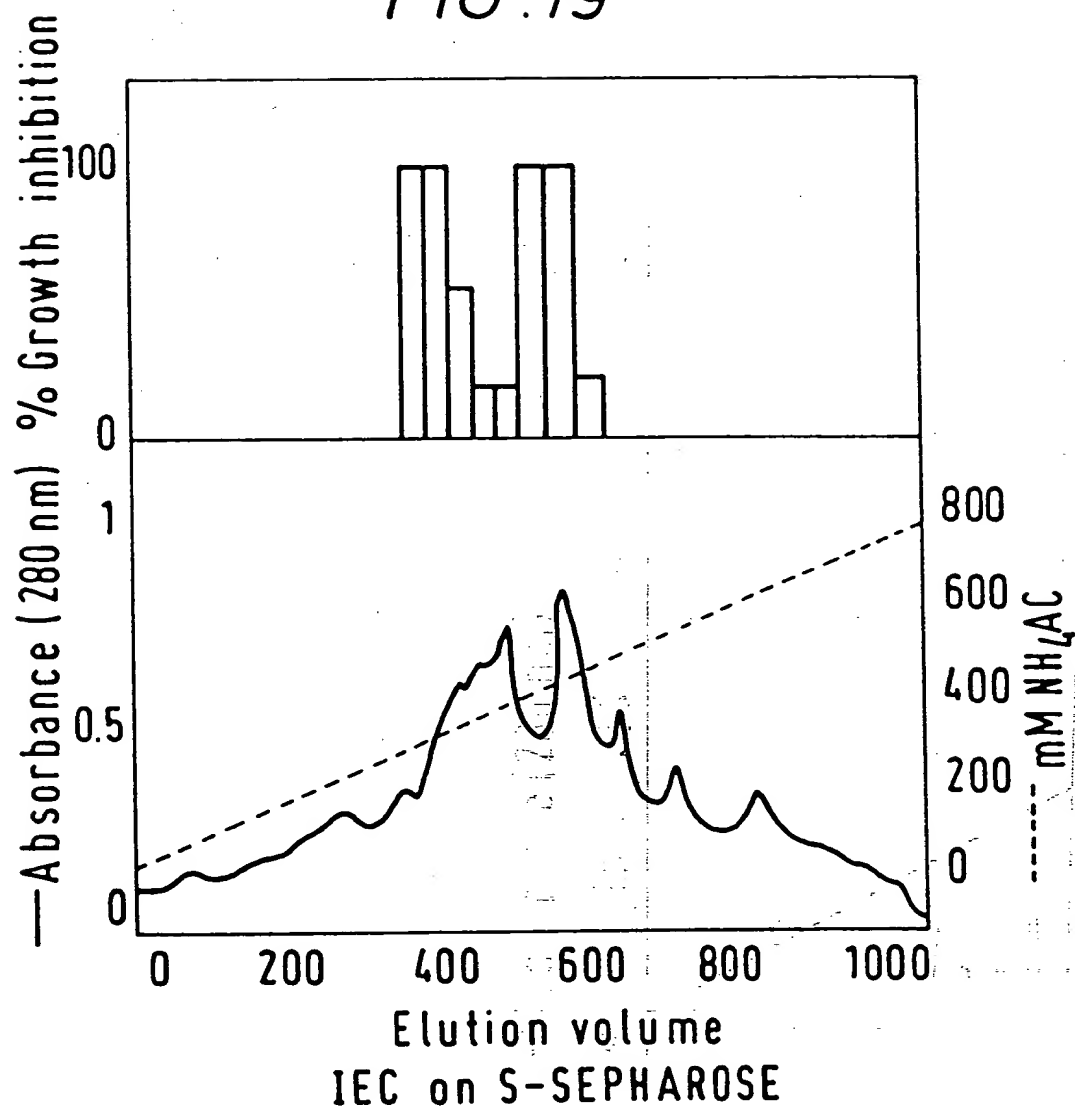


FIG. 20

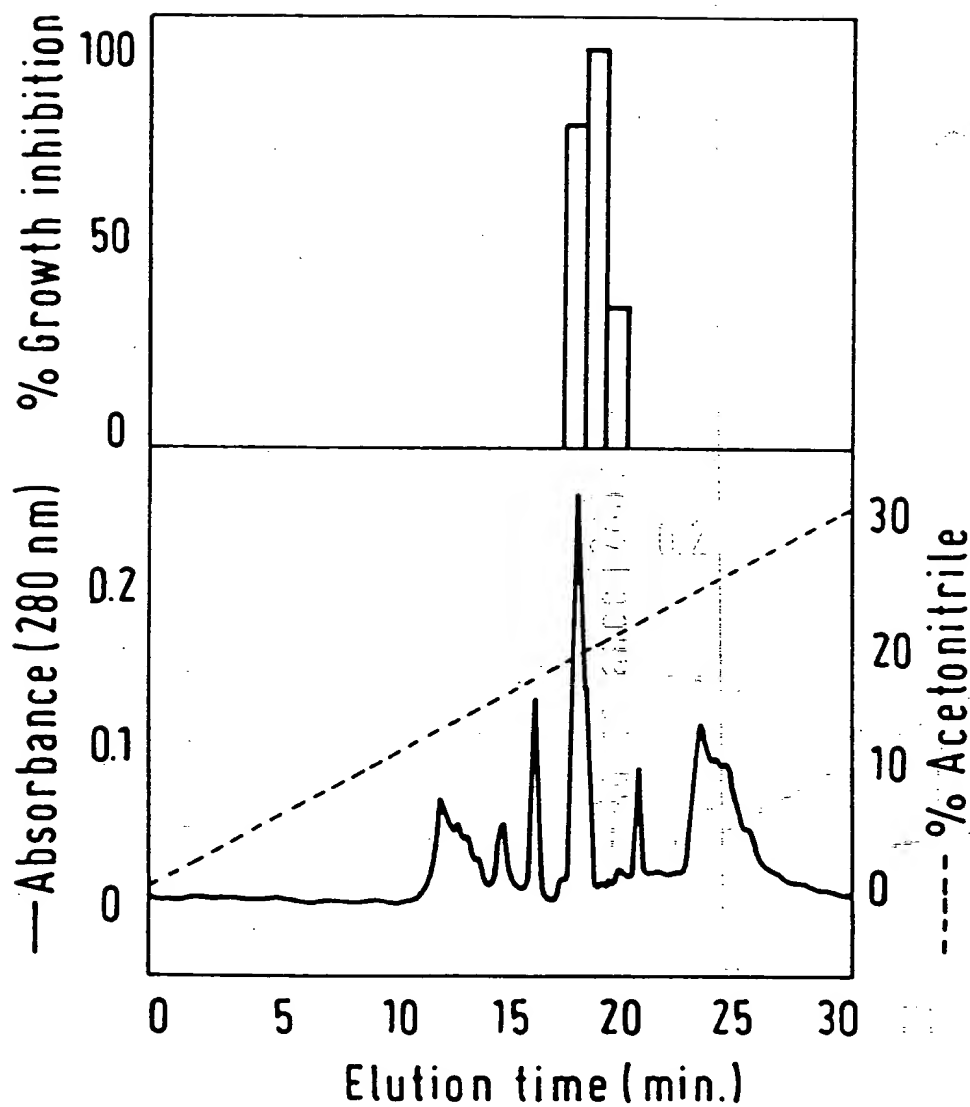


FIG. 21

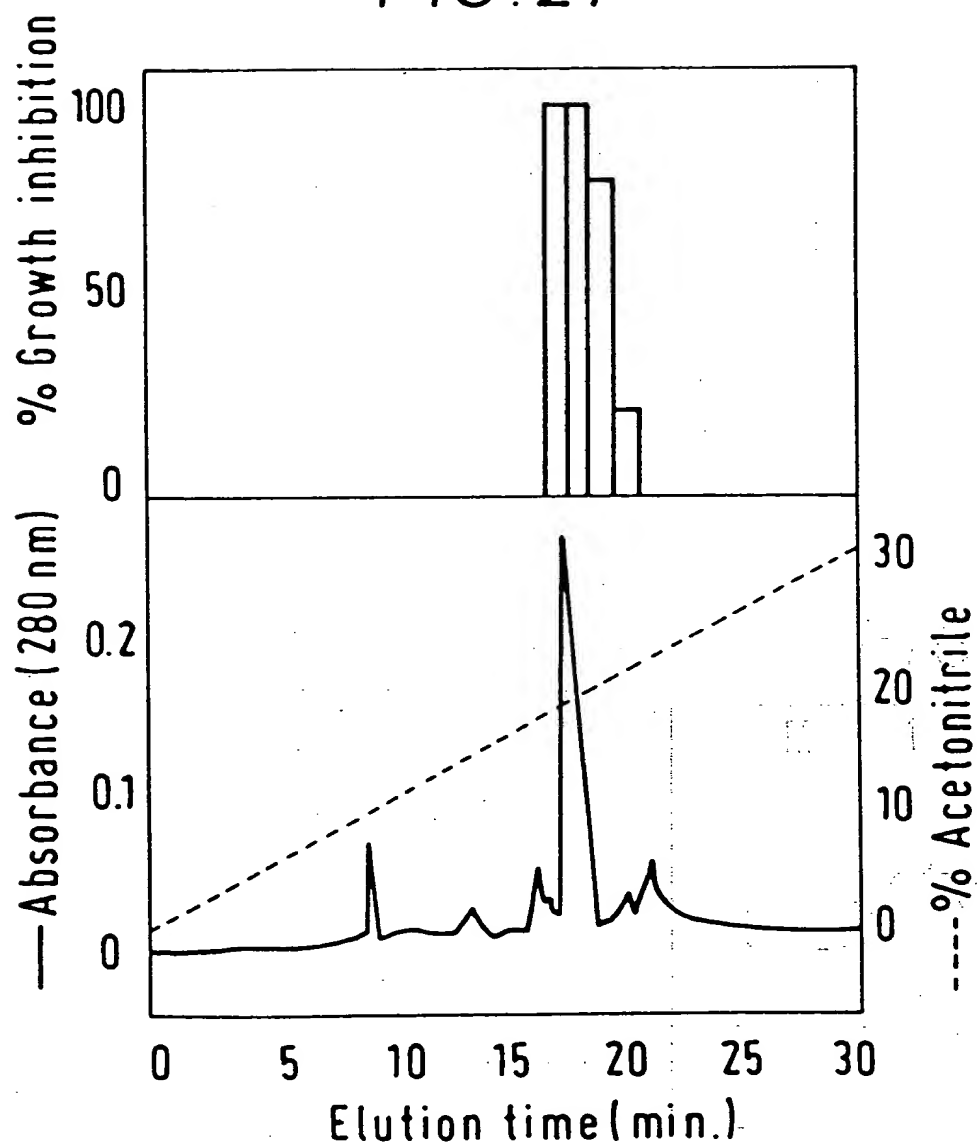


Figure 1: A schematic diagram of a 1D lattice chain. The chain consists of two parallel rows of sites. The top row has sites labeled 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20. The bottom row has sites labeled 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40. Horizontal lines connect sites in the top row to sites in the bottom row, representing nearest-neighbor interactions. Vertical lines connect sites in the top row to sites in the bottom row, representing next-nearest-neighbor interactions. The diagram is labeled 'Figure 1' at the bottom.

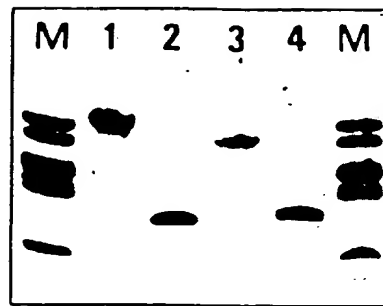


FIG. 23

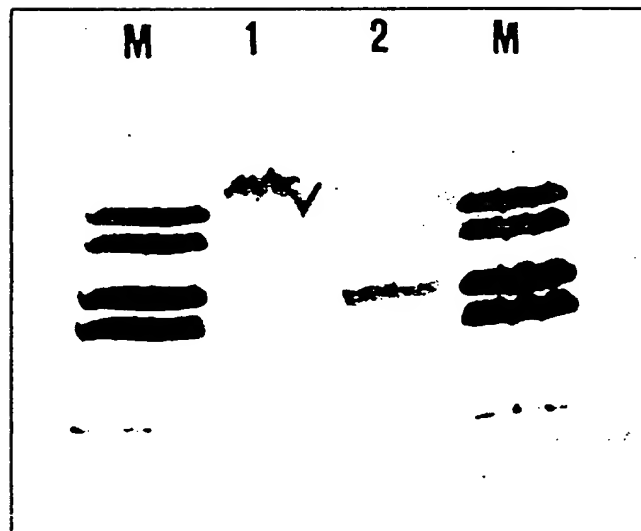


FIG. 24

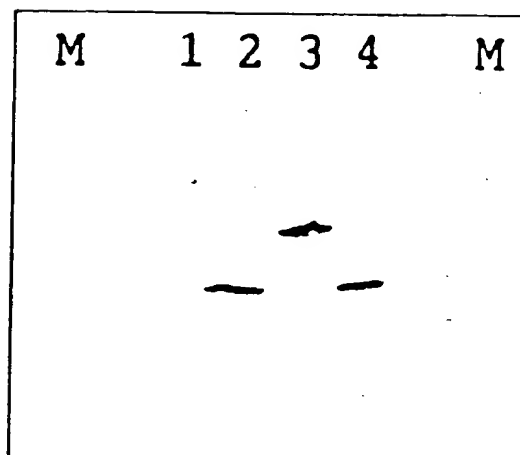


FIG. 25

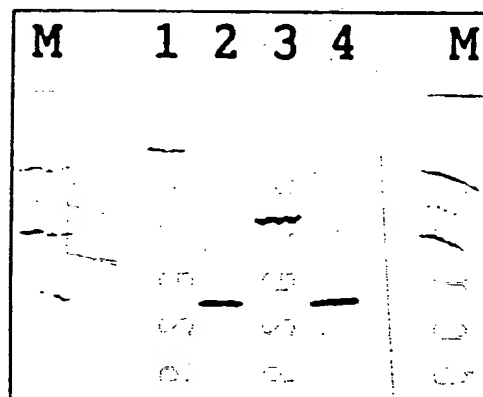


FIG. 26

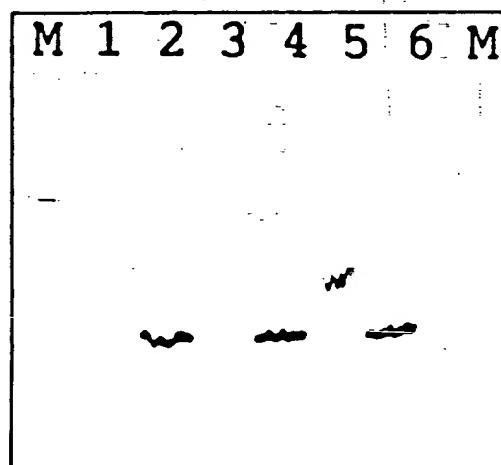




FIG. 27

Rs-AFP1 (Q) K L C E R P S G T W S G V C G N N

Rs-AFP2 (Q) K L C Q R P S G T W S G V C G N N

INACKNQCI N L E K A R H G S C N Y V F P A H K

INACKNQCI R L E K A R H G S C

Br-AFP1 . . . . .

Br-AFP2 . . . . . R

Bn-AFP1 . . . . .

Bn-AFP2 . . . . .

Sa-AFP1 . . . . .

Sa-AFP2 . . . . . R ;

At-AFP1 . . . . . S . . . . .

# FIG. 28

Dm-AMP1 E L C E K A S K T W S G N C G N T G H C D N

Dm-AMP2 E V C E K A S K T W S G N C G N T G H C

Cb-AMP1 E L C E K A S K T W S G N C G N T K H C D D

Cb-AMP2 E L C E K A S K T W S G N C G N T K H C D N

Q C K S W E G A A H G A C H V R N G K H M C F C Y F N C

Q C K S W E G A A H G A C H V R N G K H M C F C Y F N C

K C K S W E G A A H G A C H V R S G K H M C F C Y F N C

FIG. 29

LC-AFP K T C E N L S G T F K G P C I P D G N C N K H C K N

Ct-AMPI N L C E R A S L T W T G N C G N T G H C D T Q C R N

N E H L L S G R C R D D F ? - - C W C T R N C

W E S A K H G A C H K R G N W K C F C Y F D C

FIG. 30 (1/3)

Rs-AFP1 (Q)	K	L	C	E	R	P	S	G	T	W	S	G	V	C	G	N	N	A	C	
Dm-AMP1	E	L	C	E	K	A	S	K	T	W	S	G	N	C	G	N	T	G	H	C
Cb-AMP1	E	L	C	E	K	A	S	K	T	W	S	G	N	C	G	N	T	K	H	C
Cb-AMP2	E	L	C	E	K	A	S	K	T	W	S	G	N	C	G	N	T	K	H	C
Lc-AFP	K	T	C	E	N	L	S	G	T	F	K	G	P	C	I	P	D	G	N	C
Ct-AMP1	N	L	C	E	R	A	S	L	T	W	T	G	N	C	G	N	T	G	H	C
pI230	N	T	C	E	N	L	A	G	S	Y	K	G	V	C	F	G	G	-	-	C
pI39	N	T	C	E	H	L	A	D	T	Y	R	G	V	C	F	T	N	A	S	C
pSAS10	K	T	C	E	L	N	A	D	T	Y	R	G	P	C	F	T	T	G	S	C
pI322	R	H	C	E	S	L	S	H	R	F	K	G	P	C	T	R	D	S	N	C
SI $\alpha$ 2	R	V	C	M	G	K	S	A	G	F	K	G	L	C	M	R	D	Q	N	C
$\gamma$ 1pur	K	I	C	R	R	R	S	A	G	F	K	G	P	C	M	S	N	K	N	C

00750504 011201



FIG. 30 (3/3)

P	A	H	K	C	I	C	Y	F	P	C
G	K	H	M	C	F	C	Y	F	N	C
G	K	H	M	C	F	C	Y	F	N	C
G	K	H	M	C	F	C	Y	F	N	C
-	-	-	?	C	W	C	T	R	N	C
G	N	W	K	C	F	C	Y	F	D	C
-	-	-	R	C	W	C	T	K	N	C
-	-	-	K	C	F	C	T	Q	N	C
-	-	V	R	C	W	C	T	R	N	C
-	R	R	R	C	F	C	T	K	P	C
-	-	R	Q	C	K	C	I	R	Q	C
-	-	R	R	C	K	C	I	R	Q	C

00750584 014204

## FIG. 31A (1/2)

Dm-AMP1	GAG CTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC
	TGG GAG GGA GCT GCT CAT GGA GCT TGC CAT GTT AGA AAC
Dm-AMP2	GAG GTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC
Cb-AMP1	GAG CTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC
	TGG GAG GGA GCT GCT CAT GGA GCT TGC CAT GTT AGA AAC
Cb-AMP2	GAG CTT TGC GAG AAG GCT TCT AAG ACT TGG TCT GGA AAC
	TGG GAG GGA GCT GCT CAT GGA GCT TGC CAT GTT AGA TCT

GGA CAT

GGA CAT

GGA CAT

FIG. 31A (2/2)

TGC GGA AAC ACT GGA CAT TGC GAT AAC CAA TGC AAG TCT

GGA AAG CAT ATG TGC TTC TGC TAC TTC AAC TGC

TGC GGA AAC ACT GGA CAT TGC ... ..

TGC GGA AAC ACT AAG CAT TGC GAT GAT CAA TGC AAG TCT

GGA AAG CAT ATG TGC TTC TGC TAC TTC AAC TGC

TGC GGA AAC ACT AAG CAT TGC GAT AAC AAG TGC AAG TCT

GGA AAG CAT ATG TGC TTC TGC TAC TTC AAC TGC

100210040505260

100210040505260



FIG. 31B

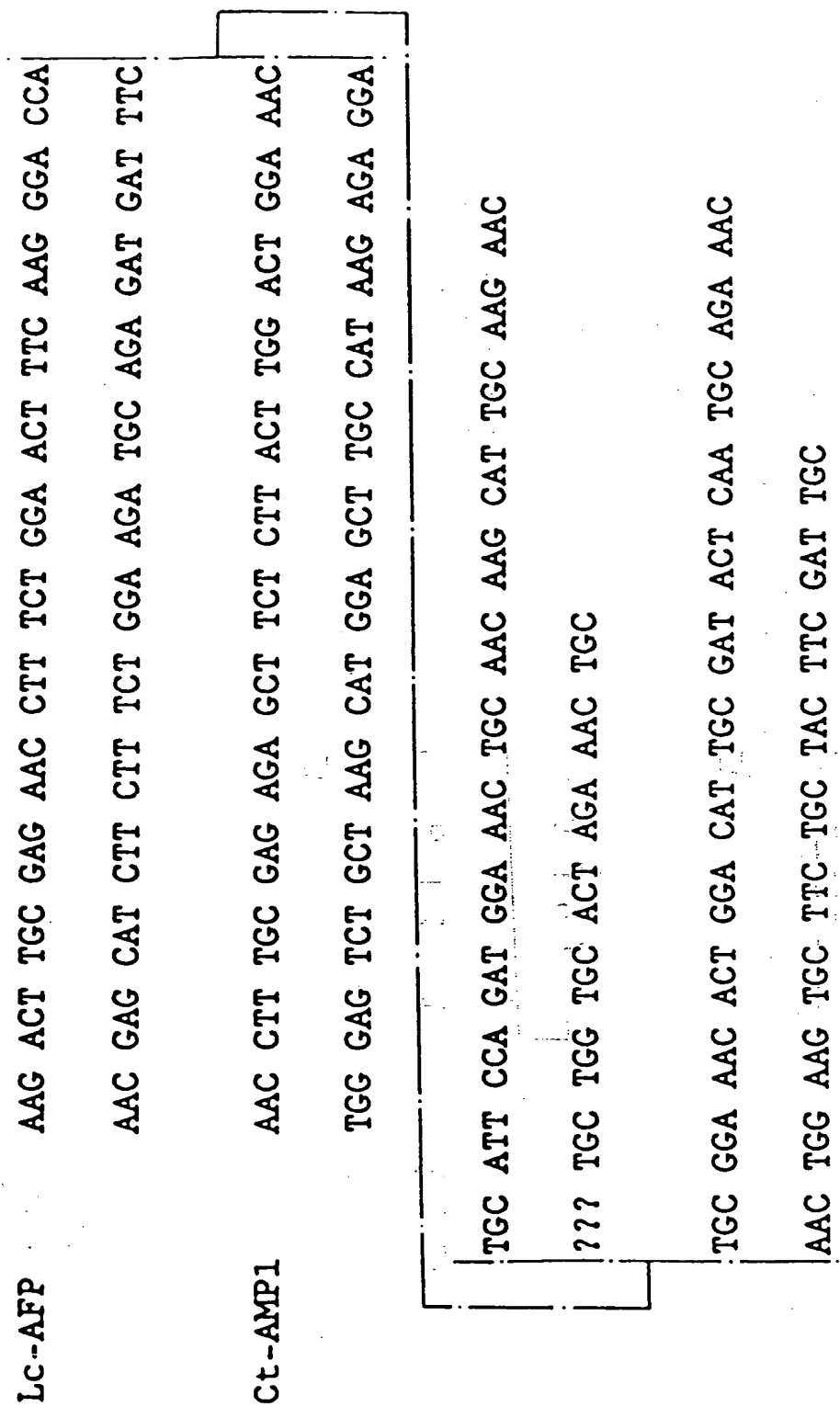


FIG. 32

Rs-nsLTP

A L S C G T V N S N L A A C I G Y L T Q

N A P L A R G C C T G V T N L N N M A ? T T P

FIG. 33 (1/2)

Rs-nsLTP

A L S C G T V N S N L A A C I G Y L T Q

So-nsLTP

G I T C G M V S S K L A P C I G Y L K G

Rc-nsLTP

V D C G Q V N S S L A S C I P F L T G

Dc-nsLTP

V L T C G Q V T G A L A P C L G Y L R S

Hv-nsLTP

A L N C G Q V D S K N K P C L T Y V Q G

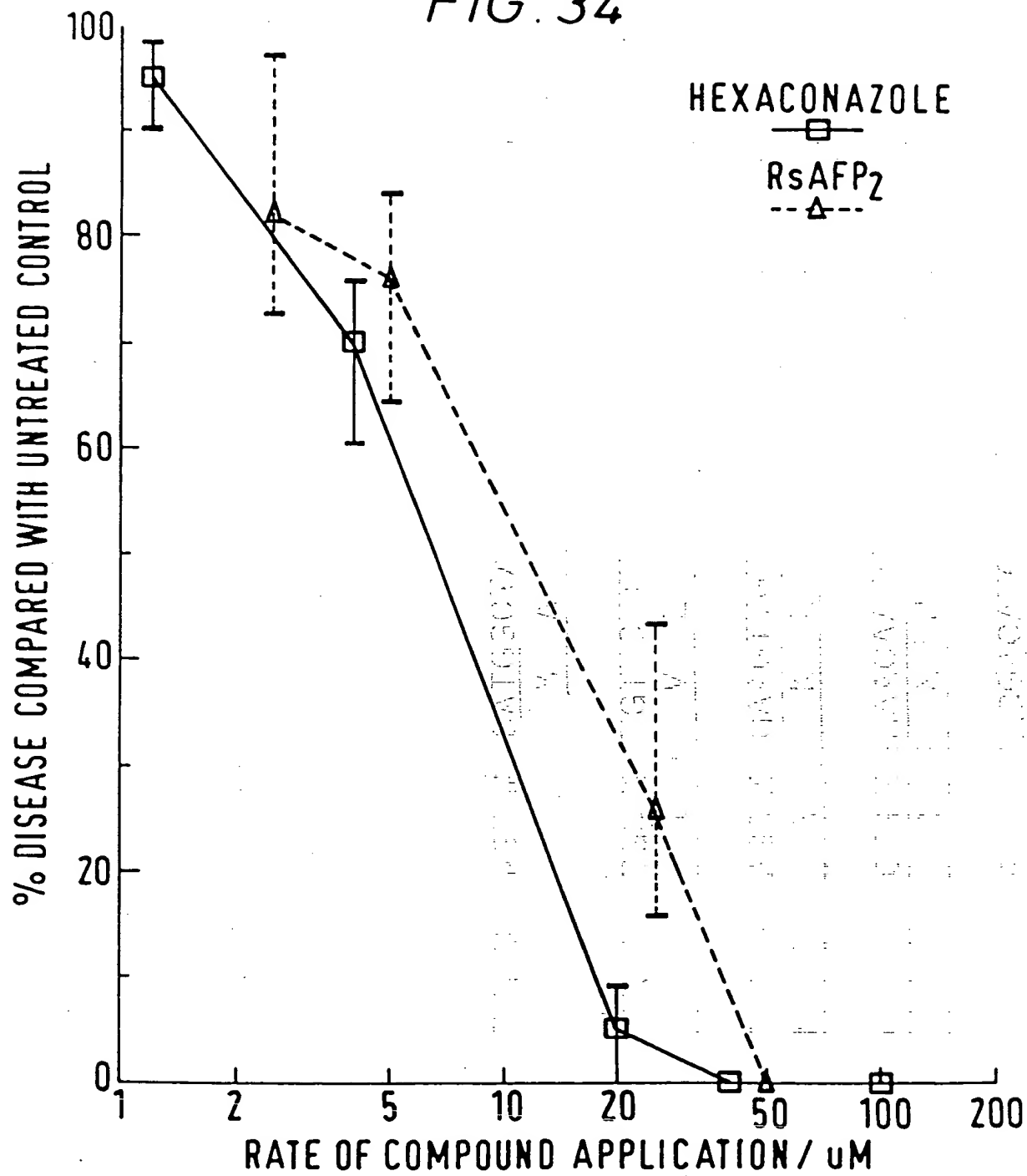
Zm-nsLTP

A I S C G Q V A S A I A P C I S Y A R G

FIG. 33 (2/2)

N - A - - -	P L A R G C C T G V T N L N N M A ?	T T P
G - - - -	P L G G S S G G I K A L N A A A A T T P	...
G V A S - -	P S A S - C C A G V Q N L K T L A P T S A	...
Q V N V P V P L T - -	C C N V V R G L N N A A R T T L	...
G P G - G - P S G L -	C C N G V R D L H N Q A Q S S G	...
Q - G S G - P S A - G	C C S G V R S L N N A A R T T A	...

FIG. 34



GTTTATTAGTGATCATGGCTAAGTTTGGTGTCATCATCGCACTT 45  
M A K F A S I I A L

CTTTTGGCTGCTCTGTTCITTTTGGCTGCTTTCGAAGCACCAACA 90  
L F A A L V L F A A F E A E T

ATGGTGGAAGCACAGAAAGTTGTGCGAAAGGCCAAGTGGGACATGG 135  
M V E A Q K L C E R P S G T W

TCAGGAGTCTGTGGAACAATAACGCATGCAAGAATCAGTGCATT 180  
S G V C G N N N A C K N Q C I

AACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225  
N L E K A R H G S C N Y V F P

GCTCACAAGTGATCTGCTACTTTCCTTGTIAATTATCGCAAAC 270  
A H K C I C Y F P C \*

TCTTTGGTGAATAGTTTTTATGTAATTTACACAAATAAGTCAGT 315

GTCACATCCATGAGTGATTTTAAGACATGTACCAGATATGTTAT 360

GTTGGTTCGGTTATACAAATAAAGTTTTTATTCACCAAAAAAAA 405

FIG. 35

AAAAAAA

FIG. 36

GGAAATAACGCATGCAAGAAATCAGTGCAATTCGACTTGAGAAA	45
G N N A C K N Q C I R L E K	
GCACGACATGGGTCTTGCAACTATGTCTTCCCAGCTCACAAGTGT	90
A R H G S C N Y V F P A H K C	
ATCTGTTATTTCCCTTGTIAA <u>TTCCATAAACTCTTCGGTGGTTAA</u>	135
I C Y F P C *	
TAGTGCGGCATATTACATATAATTAATAAGTTTGTCACACTATT	180
TATTAGTGACTTTATGACATGTGCCAGGTATGTTTATGTTGGGTT	225
GGTGTAAATAAAAAAGTTCACGGATAATAAGATGATAAGCTCA	270
CGTCGCCAAAAAA	284

10210 1855260

FIG. 37 (1/2)

CCCCGGGCTGCAG

GAATTCGGGGCCGC

10 20 30 40 50 60  
| | | | |  
GTTTATTAGTCATCGGCTAAGTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTT

M A K F A S I I A L L F A A L

70 80 90 100 110 120  
| | | | |  
GTTCTTTTGCTGCTTTTCGAAGCACCAACAATGGTGAAGCACAGAAAGTTGTGCCAAAGG

V L F A A F E A P T M V E A Q K L C Q R





FIG. 38

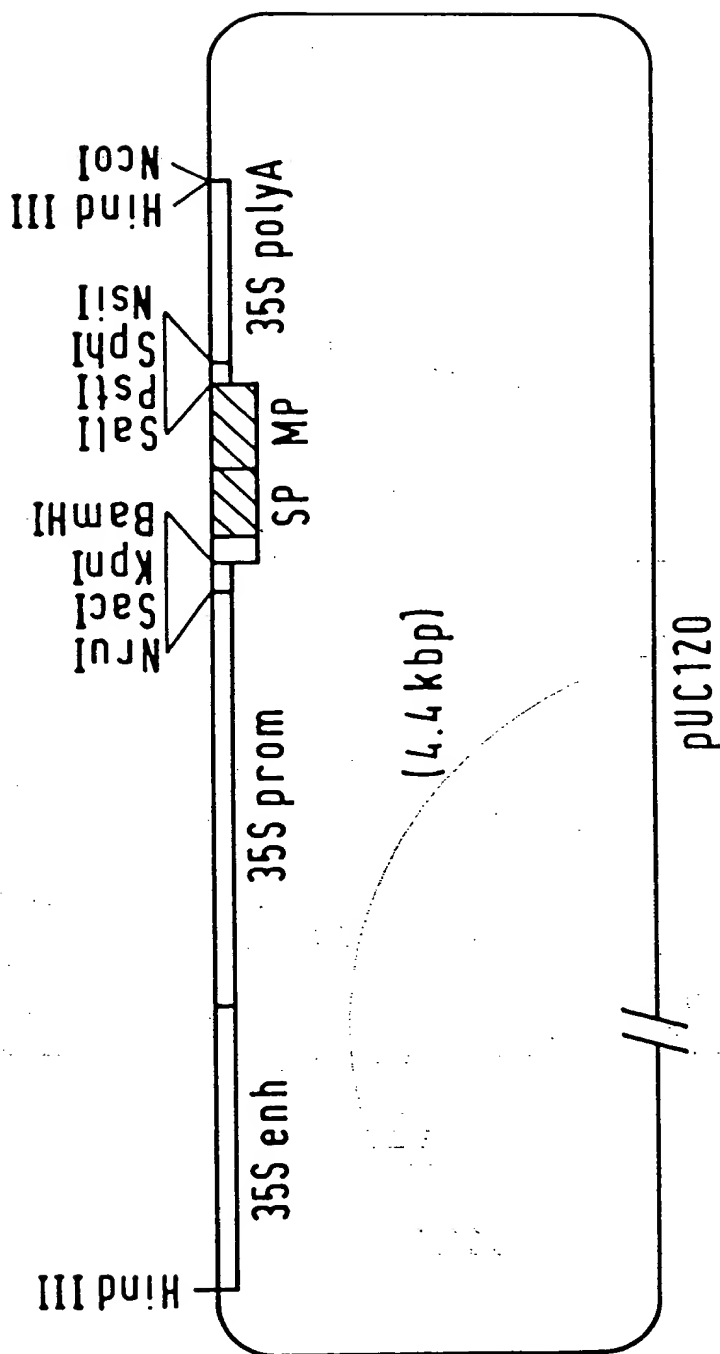


FIG. 39

